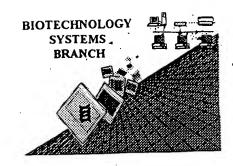
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09700158Source: 0IPEDate Processed by STIC: 08/15/200/

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

	C 17 00 : -12
ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/700 15 8
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOI	
Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in Patentln version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

DATE: 08/15/2001

TIME: 07:36:46

OIPE

```
Input Set : A:\Seq.txt
                      Output Set: N:\CRF3\08132001\1700158.raw
                                                                          Does Not Comply
      3 <110> APPLICANT: BOWNESS, RACHEL
                                                                     Corrected Diskette Needed
              MCMICHAEL, PAUL
                                                                           supreger I and 2
              JAMES, ANDREW
      7 <120> TITLE OF INVENTION: NOVEL MOLECULE AND DIAGNOSTIC METHOD
      9 <130> FILE REFERENCE: P02077US0/10025595
     11 <140> CURRENT APPLICATION NUMBER: 09/700,158
     12 <141> CURRENT FILING DATE: 2000-11-10
     14 <150> PRIOR APPLICATION NUMBER: PCT/GB9901481
     15 <151> PRIOR FILING DATE: 1999-05-11
     17 <160> NUMBER OF SEQ ID NOS: 9
     19 <170> SOFTWARE: PatentIn version 3.0
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 9
     23 <212> TYPE: PRT
     24 <213> ORGANISM: INFLUENZA
     26 <400> SEQUENCE: 1
     28 Ser Arg Tyr Trp Ala Ile Arg Thr Arg
     29 1
     31 <210> SEQ ID NO: 2
     32 <211> LENGTH: 10
     33 <212> TYPE: PRT
     34 <213> ORGANISM: HIV
     36 <400> SEQUENCE: 2
     38 Lys Arg Trp Ile Ile Met Gly Leu Asn Lys
     41 <210> SEQ ID NO: 3
     42 <211> LENGTH: 17
                                               Errored. The appropriate 213 response is Artificial Sequence
     43 <212> TYPE: PRT
C--> 44 <213> ORGANISM: ARTIFICIAL PEPTIDE
     46 <220> FEATURE:
     47 <221> NAME/KEY: misc_feature
     48 <222> LOCATION: (1)..(17)
     49 <223> OTHER INFORMATION: Biotinylation Sequence ^{oldsymbol{t}}
     52 <400> SEQUENCE: 3
     54 Gly Ser Leu His His Ile Leu Asp Ala Gln Lys Met Val Trp Asn His
     55 1
     57 Arg
     59 <210> SEO ID NO: 4
     60 <211> LENGTH: 9
     61 <212> TYPE: PRT
     62 <213> ORGANISM: CMV (HLA-A2 CMV)
     64 <400> SEQUENCE: 4
     66 Asn Leu Val Pro Met Val Ala Thr Val
     67 1
     69 <210> SEQ ID NO: 5
     70 <211> LENGTH: 26
     71 <212> TYPE: DNA
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/700,158

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```
Input Set : A:\Seq.txt
                     Output Set: N:\CRF3\08132001\1700158.raw
C--> 72 <213> ORGANISM: ARTIFICIAL
     75 <220> FEATURE:
     76 <221> NAME/KEY: misc feature
     77 <222> LOCATION: (1)..(26)
     78 <223> OTHER INFORMATION: DNA primer {\cal U}
     81 <400> SEQUENCE: 5
                                                                                  26
     82 gagacacaga tcagcaaggc caaggc
     85 <210> SEQ ID NO: 6
     86 <211> LENGTH: 26
     87 <212> TYPE: DNA
C--> 88 <213> ORGANISM: ARTIFICIAL \cup
     91 <220> FEATURE:
     92 <221> NAME/KEY: misc feature
     93 <222> LOCATION: (1)..(26)
     94 <223> OTHER INFORMATION: DNA Primer (
     97 <400> SEQUENCE: 6
     98 gccttggcct tgctgatctg tgtctc
     101 <210> SEQ ID NO: 7
                                      DNA is by definition a nucleotide sequence
     102 <211> LENGTH: 21
     103 <212> TYPE: (DŃA')
C--> 104 <213> ORGANISM: ARTIFICIAL
     107 <220> FEATURE:
     108 <221> NAME/KEY: misc feature
                                                     peptide sequence and have fuited
to describe your artifreral nucleotide
sequence in field 223.
     109 <222> LOCATION: (1)..(21)
     110 <223> OTHER INFORMATION: ARTIFICIAL PEPTIDE
     113 <400> SEQUENCE: 7
     114 tttqttqaat tcaggaggaa t
     117 <210> SEQ ID NO: 8
     118 <211> LENGTH: 67
     119 <212> TYPE: DNA
C--> 120 <213> ORGANISM: ARTIFICIAL
     123 <220> FEATURE:
     124 <221> NAME/KEY: misc feature
     125 <222> LOCATION: (1)..(67)
     126 <223> OTHER INFORMATION: DNA Primer
     129 <400> SEQUENCE: 8
     130 cggggagtgg gactctaccc tccctaggga cgtagtataa gacctacgtg tcttttacca
                                                                                   60
                                                                                   67
     132 cacctta
     135 <210> SEQ ID NO: 9
     136 <211> LENGTH: 22
     137 <212> TYPE: PRT
C--> 138 <213> ORGANISM: ARTIFICIAL
     141 <220> FEATURE:
     142 <221> NAME/KEY: misc feature
     143 <222> LOCATION: (1)..(22)
     144 <223> OTHER INFORMATION: Fusion protein
     147 <400> SEQUENCE: 9
     149 Pro Leu Thr Leu Arg Trp Glu Gly Ser Leu His His Ile Leu Asp Ala
     150 1
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/700,158

RAW SEQUENCE LISTING

DATE: 08/15/2001

PATENT APPLICATION: US/09/700,158

TIME: 07:36:46

Input Set : A:\Seq.txt
Output Set: N:\CRF3\08132001\I700158.raw

152 Gln Lys Met Val Trp Asn

VERIFICATION SUMMARY

DATE: 08/15/2001

PATENT APPLICATION: US/09/700,158

TIME: 07:36:47

Input Set : A:\Seq.txt

Output Set: N:\CRF3\08132001\I700158.raw

L:44 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:72 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:88 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:104 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:120 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:138 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9